

FIGURE 1

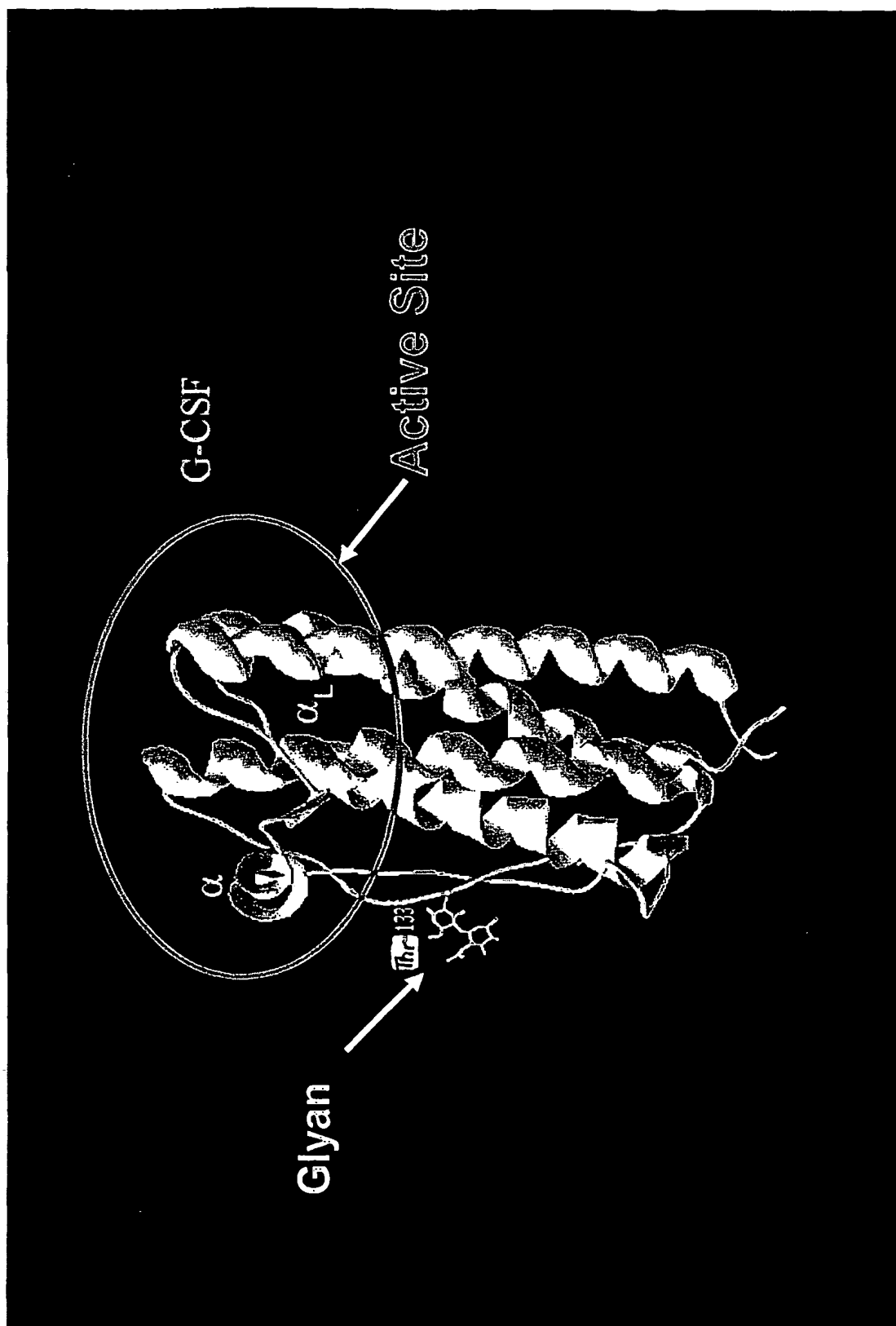


FIGURE 2

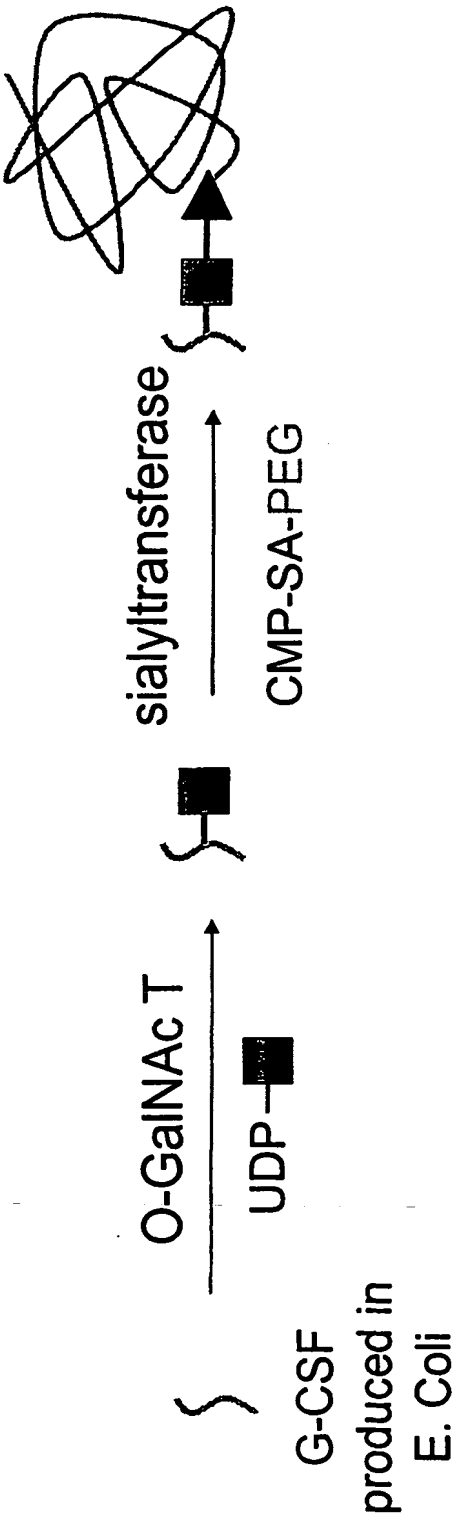


FIGURE 3

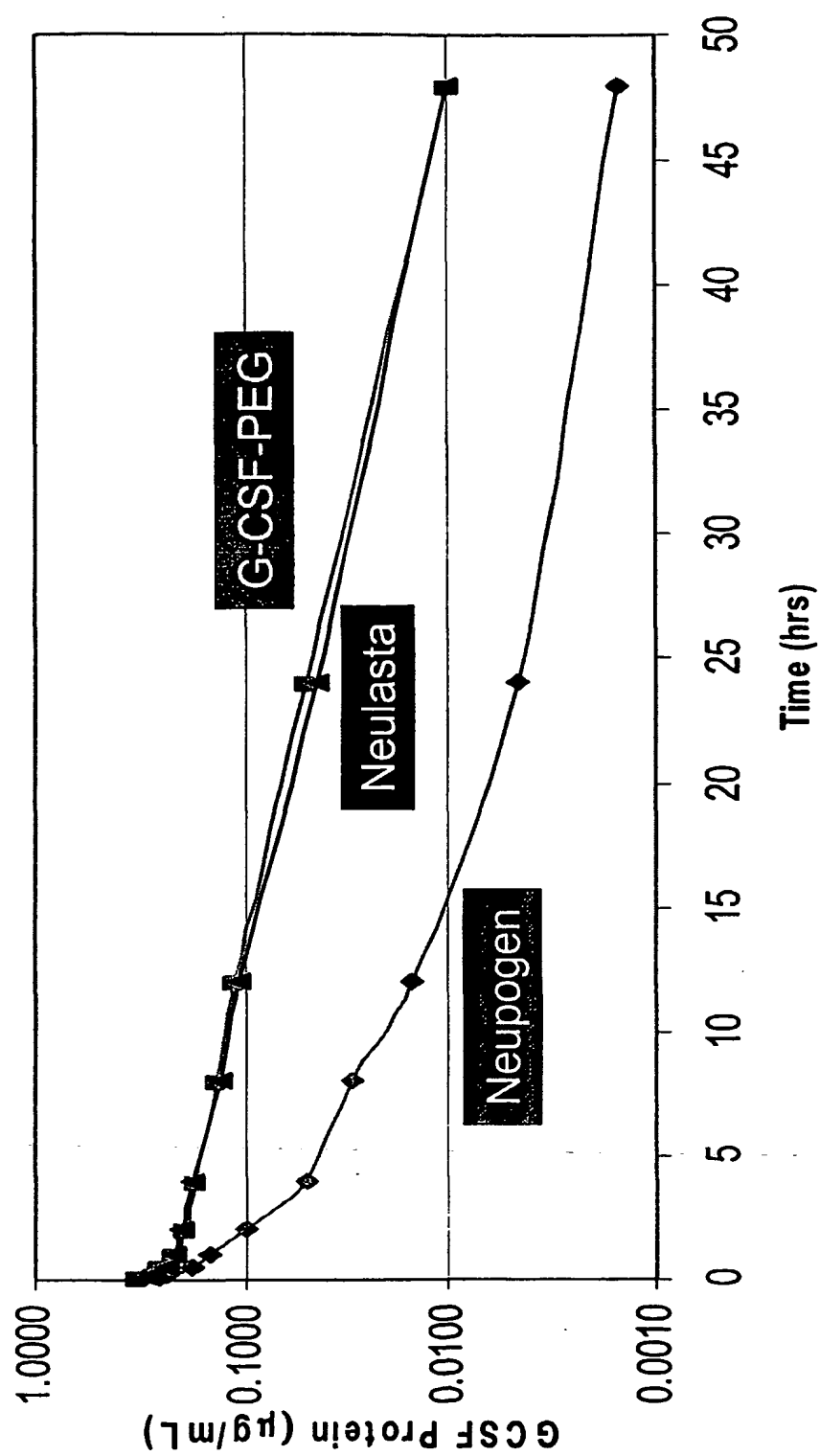
IV Bolus injection of [ $^{125}$ I]-labeled proteins in rats

FIGURE 4

Mouse WBC Response to G-CSF Variants (250  $\mu\text{g}/\text{Kg}$ )  
Administered i.v. at 0 hours

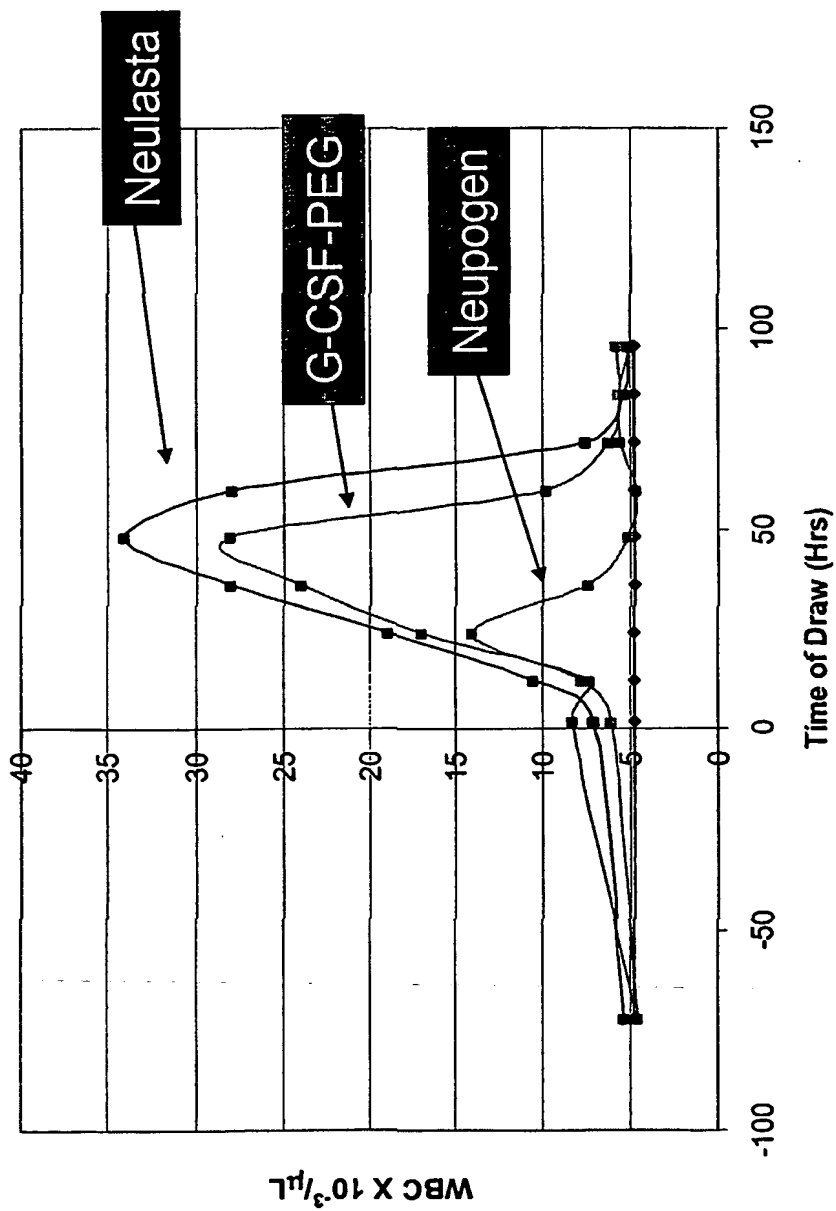
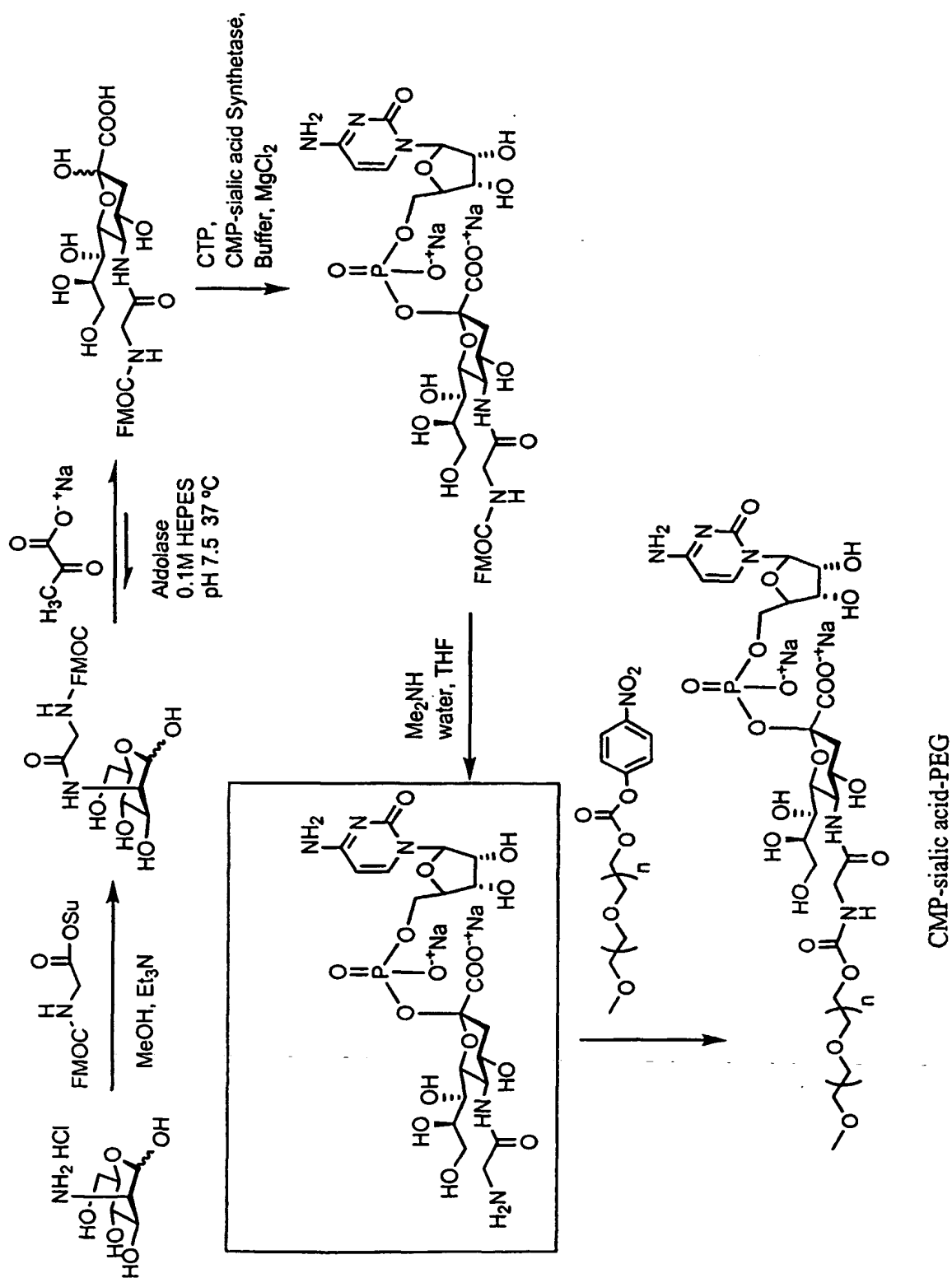


FIGURE 5



**FIGURE 6****175 amino acid variant**

MTPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLCA  
TYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLS  
QLHSGLFLYQGILLQALEGISPELGPTLDTLQLDVADFAT  
TIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVL  
VASHLQSFLEVSYRVLRLAQP (SEQ ID NO: 1).

**174 amino acid variant**

TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLCA  
TYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLS  
QLHSGLFLYQGILLQALEGISPELGPTLDTLQLDVADFATTI  
WQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLV  
VASHLQSFLEVSYRVLRLAQP (SEQ ID NO: 2).

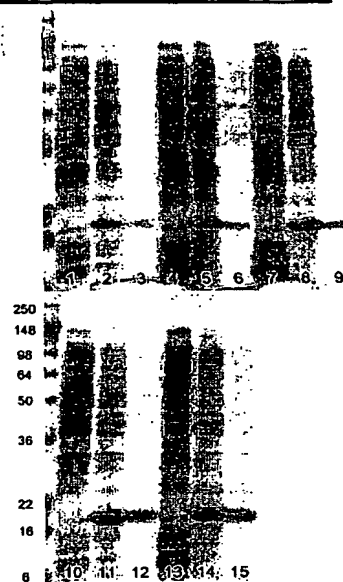
FIGURE 7

## Testing growth conditions – washing IBs

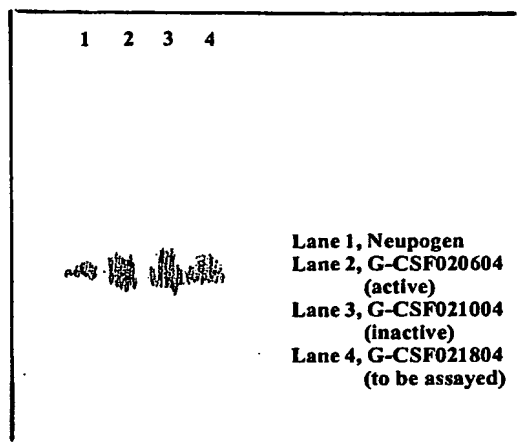
37°C, 1mM (final) IPTG				IB yields (~0.7-1g/L)
	Media	Buffered pH	Time	wet IB pellet (mg)
1.	LB	n/a	5hr	120
2.	TB	7.4 (K-PO <sub>4</sub> )	5hr	230
3.	TB	6 (MES)	5hr	170
4.	LB	n/a	o/n	190
5.	TB	7.4 (K-PO <sub>4</sub> )	o/n	250

Cell samples, loaded equally by  $\mu$ g  
(better expression of overnights more apparent)

- |                      |                       |
|----------------------|-----------------------|
| 1. #1 lysate, supe   | 10. #4 lysate, supe   |
| 2. #1 lysate, pellet | 11. #4 lysate, pellet |
| 3. #1 final IB       | 12. #4 final IB       |
| 4. #2 lysate, supe   | 13. #5 lysate, supe   |
| 5. #2 lysate, pellet | 14. #5 lysate, pellet |
| 6. #2 final IB       | 15. #5 final IB       |
| 7. #3 lysate, supe   |                       |
| 8. #3 lysate, pellet |                       |
| 9. #3 final IB       |                       |



Purified IB's are shown in lanes 3, 6, 9, 12 and 15. Note IB lanes loaded at approximately  $\frac{1}{2}$  the amount of the preceding lane (based on predicted pellet weight).

**FIGURE 8****Western Blot Analysis of Refolded G-CSF  
Native Polyacrylamide Gel Electrophoresis**

G-CSF020604 and G-CSF021004 came from the same batch of refolding reaction. The only difference was that G-CSF021004 was saved from the flowthrough of G-CSF020604 by adjusting pH and reloading onto SP Sepharose. G-CSF021804 was a separate refolding batch.

After SP-sepharose you see only one band by Coomassie stain or Western.



FIGURE 9

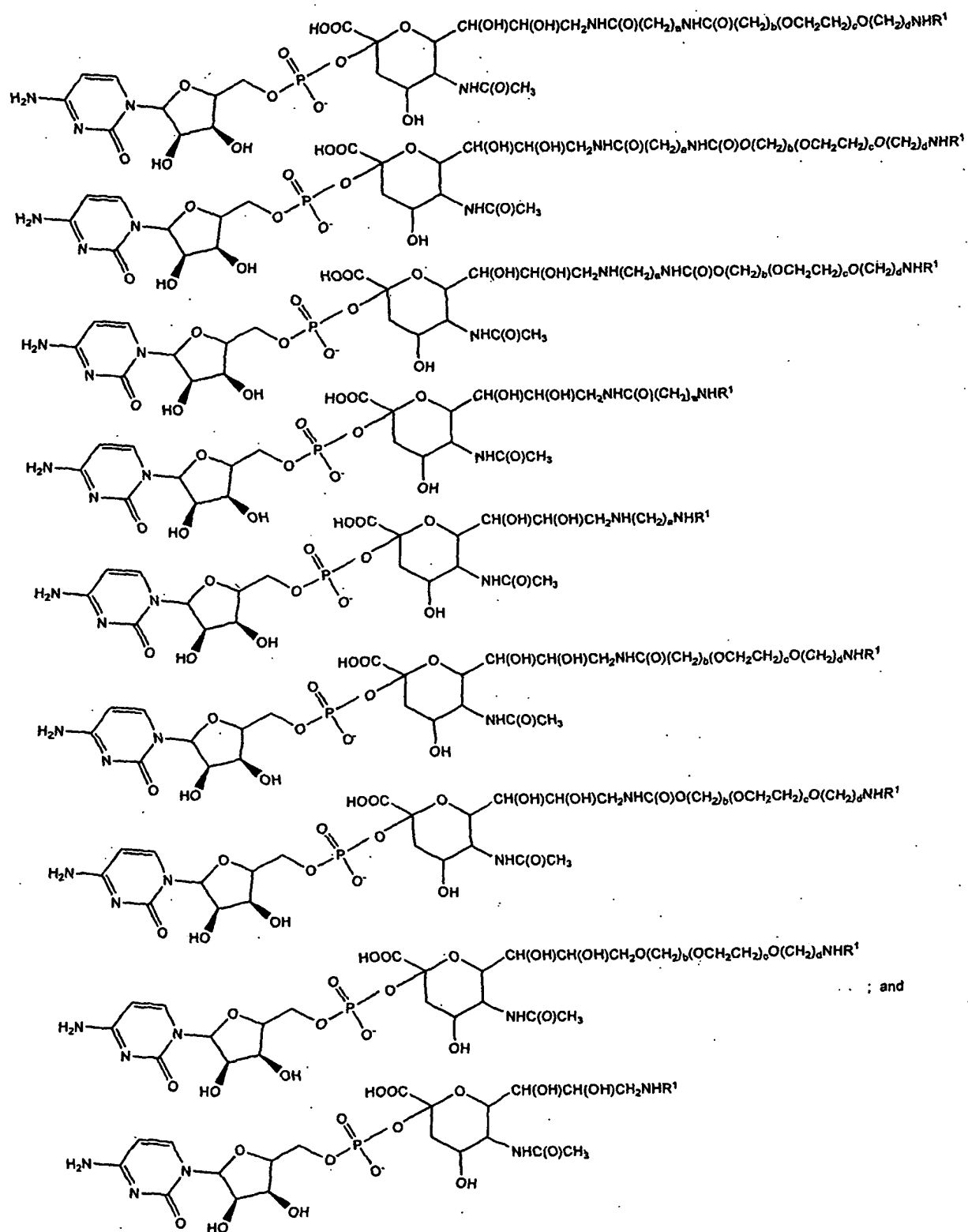


FIGURE 10

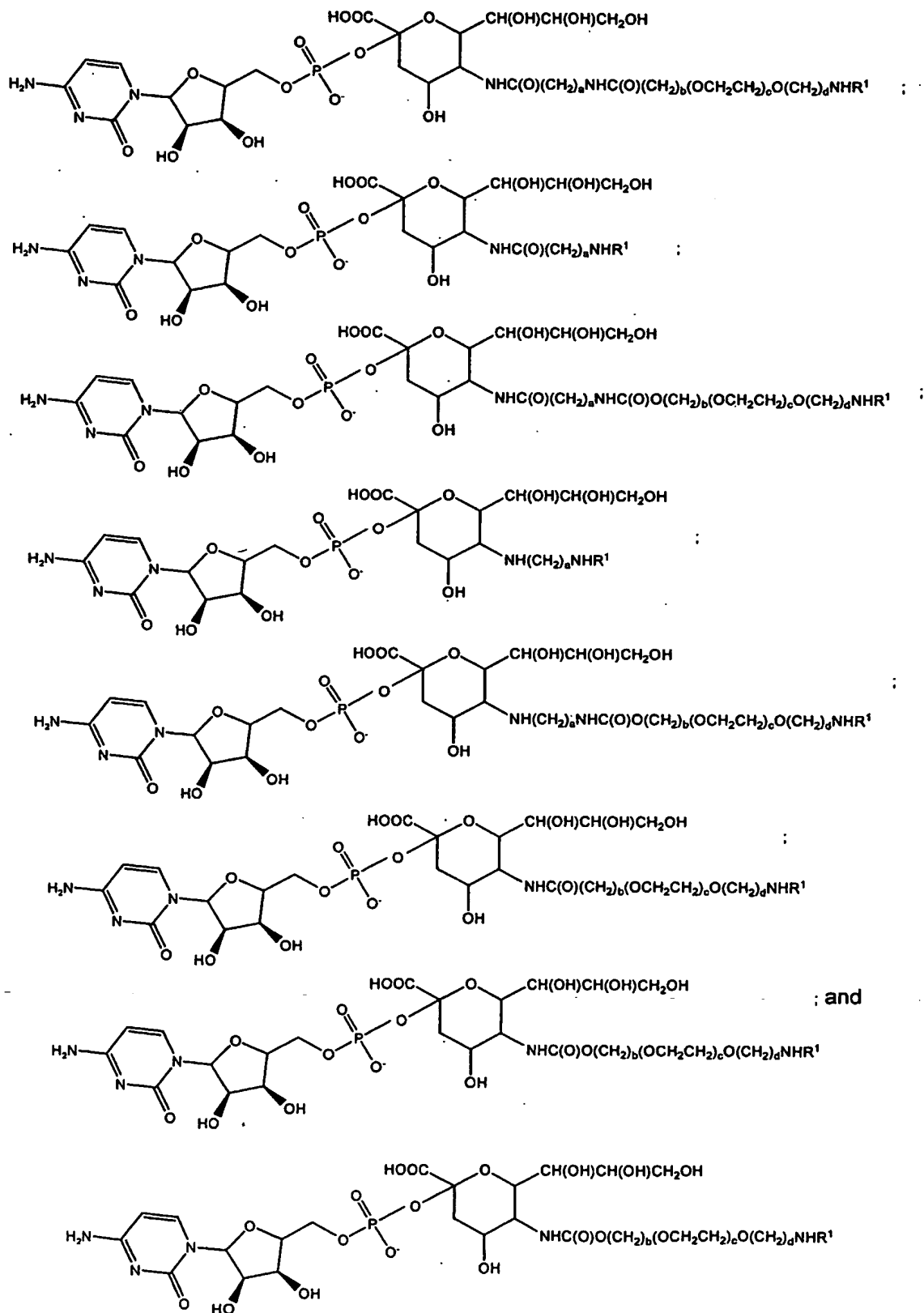


FIGURE 11A

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
At1g08280	<i>Arabidopsis thaliana</i>	n.d.	AC011438 AAF18241.1 BT004583 AAF042829.1 NC_003070 NP_172305.1	Q81W00 Q9SGD2	
At1g08660/F22O13.14	<i>Arabidopsis thaliana</i>	n.d.	AC003981 AAF99778.1 AY064135 AAL36042.1 AY124807 AAM70516.1 NC_003070 NP_172342.1 NM_180609 NP_850940.1	Q8VZJ0 Q9FRR9	
At3g48820/T21J18_90	<i>Arabidopsis thaliana</i>	n.d.	AY080589 AAL85966.1 AY133816 AAM91750.1 AL132963 CAB87910.1 NM_114741 NP_190451.1	Q8RY00 Q9M301	
$\alpha$ -2,3-sialyltransferase (ST3Gal-IV)	<i>Bos taurus</i>	n.d.	AJ584673 CAE48298.1		
$\alpha$ -2,3-sialyltransferase (ST3Gal-V)	<i>Bos taurus</i>	n.d.	AJ585768 CAE51392.1		
$\alpha$ -2,6-sialyltransferase (Siat7b)	<i>Bos taurus</i>	n.d.	AJ620651 CAF05850.1		
$\alpha$ -2,8-sialyltransferase (Siat8A)	<i>Bos taurus</i>	2.4.99.8	AJ699418 CAG27880.1		
$\alpha$ -2,8-sialyltransferase (Siat8D)	<i>Bos taurus</i>	n.d.	AJ699421 CAG27883.1		
$\alpha$ -2,8-sialyltransferase ST8Sia-III (Siat8C)	<i>Bos taurus</i>	n.d.	AJ704563 CAG28696.1		
CMP $\alpha$ -2,6-sialyltransferase (ST6Gal I)	<i>Bos taurus</i>	2.4.99.1	Y15111 CAA75385.1 NM_177517 NP_803483.1	O18974	
sialyltransferase 8 (fragment)	<i>Bos taurus</i>	n.d.	AF450088 AAL47018.1	Q8WN13	
sialyltransferase ST3Gal-II (Siat4B)	<i>Bos taurus</i>	n.d.	AJ748841 CAG44450.1		
sialyltransferase ST3Gal-III (Siat6)	<i>Bos taurus</i>	n.d.	AJ748842 CAG44451.1		
sialyltransferase ST3Gal-VI (Siat10)	<i>Bos taurus</i>	n.d.	AJ748843 CAG44452.1		
ST3Gal-III	<i>Bos taurus</i>	n.d.	AJ305086 CAC24698.1	Q9BEG4	
ST6GalNAc-VI	<i>Bos taurus</i>	n.d.	AJ620949 CAF06586.1		
CDS4	<i>Branchiostoma floridae</i>	n.d.	AF391289 AAM18873.1	Q8T771	
polysialyltransferase (PST) (fragment) ST8Sia IV	<i>Cercopithecus aethiops</i>	2.4.99.-	AF210729 AAF17105.1	Q9TT09	
polysialyltransferase (STX) (fragment) ST8Sia II	<i>Cercopithecus aethiops</i>	2.4.99.-	AF210318 AAF17104.1	Q9TT10	
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Ciona intestinalis</i>	n.d.	AJ626815 CAF25173.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat4)	<i>Ciona savignyi</i>	n.d.	AJ626814 CAF25172.1		
$\alpha$ -2,8-polysialyltransferase ST8Sia IV	<i>Cricetulus griseus</i>	2.4.99.-	-AAE28634 Z46801 CAA86822.1	Q64690	
Gal $\beta$ -1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase ST3Gal I	<i>Cricetulus griseus</i>	n.d.	AY266675 AAP22942.1	Q80WK0	
Gal $\beta$ -1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase ST3Gal II (fragment)	<i>Cricetulus griseus</i>	n.d.	AY266676 AAP22943.1	Q80WK9	
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Danio rerio</i>	n.d.	AJ783740 CAH04017.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5)	<i>Danio rerio</i>	n.d.	AJ783741 CAH04018.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Danio rerio</i>	n.d.	AJ626821 CAF25179.1		
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat4c)	<i>Danio rerio</i>	n.d.	AJ744809 CAG32845.1		

FIGURE 11B

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat5-related)	<i>Danio rerio</i>	n.d.	AJ783742 CAH04019.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I (Siat1)	<i>Danio rerio</i>	n.d.	AJ744801 CAG32837.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Danio rerio</i>	n.d.	AJ634459 CAG25680.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Danio rerio</i>	n.d.	AJ646874 CAG26703.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Danio rerio</i>	n.d.	AJ646883 CAG26712.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	<i>Danio rerio</i>	n.d.	AJ715535 CAG29374.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Danio rerio</i>	n.d.	AJ715543 CAG29382.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IV (Siat 8D) (fragment)	<i>Danio rerio</i>	n.d.	AJ715545 CAG29384.1		
$\alpha$ -2,8-sialyltransferase ST8Sia V (Siat 8E) (fragment)	<i>Danio rerio</i>	n.d.	AJ715546 CAG29385.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	<i>Danio rerio</i>	n.d.	AJ715551 CAG29390.1		
$\beta$ -galactosamide $\alpha$ -2,6- sialyltransferase II (ST6Gal II)	<i>Danio rerio</i>	n.d.	AJ627627 CAF29495.1		
<i>N</i> -glycan $\alpha$ -2,8- sialyltransferase	<i>Danio rerio</i>	n.d.	BC050483 AAH50483.1 AY055462 AAL17875.1 NM_153662 NP_705948.1	Q7ZU51 Q8QH83	
ST3Gal III-related (sial6r)	<i>Danio rerio</i>	n.d.	BC053179 AAH53179.1 AJ626820 CAF25178.1 NM_220355 NP_956649.1	Q7T3B9	
ST3Gal-V	<i>Danio rerio</i>	n.d.	AJ619960 CAF04061.1		
st6GalNAc-VI	<i>Danio rerio</i>	n.d.	BC060932 AAH60932.1 AJ620947 CAF06584.1		
$\alpha$ -2,6-sialyltransferase (CG4871) ST6Gal I	<i>Drosophila melanogaster</i>	2.4.99.1	AE003465 AAF47256.1 AF218237 AAG13185.1 AF397532 AAK92126.1 AE003465 AAM70791.1 NM_079129 NP_523853.1 NM_166684 NP_726474.1	Q9GU23 Q9W121	
$\alpha$ -2,3-sialyltransferase (ST3Gal-VI)	<i>Gallus gallus</i>	n.d.	AJ585767 CAE51391.1 AJ627204 CAF25503.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>Gallus gallus</i>	2.4.99.4	X80503 CAA56666.1 NM_205217 NP_990548.1	Q11200	
$\alpha$ -2,3-sialyltransferase ST3Gal IV (fragment)	<i>Gallus gallus</i>	2.4.99.-	AF035250 AAC14163.1	Q73724	
$\alpha$ -2,3-sialyltransferase (ST3GAL-II)	<i>Gallus gallus</i>	n.d.	AJ585761 CAE51385.2		
$\alpha$ -2,6-sialyltransferase (Siat7b)	<i>Gallus gallus</i>	n.d.	AJ620653 CAF05852.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Gallus gallus</i>	2.4.99.1	X75558 CAA53235.1 NM_205241 NP_990572.1	Q92182	
$\alpha$ -2,6-sialyltransferase ST6GalNAc I	<i>Gallus gallus</i>	2.4.99.3	AAE68028.1 AAE68029.1 X74946 CAA52902.1 NM_205240 NP_990571.1	Q92183	
$\alpha$ -2,6-sialyltransferase ST6GalNAc II	<i>Gallus gallus</i>	2.4.99.-	X77775 AAE68030.1 NM_205233 CAA54813.1 NP_990564.1	Q92184	
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (SIAT7C)	<i>Gallus gallus</i>	n.d.	AJ634455 CAG25677.1		

FIGURE 11C

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
(fragment) $\alpha$ -2,6-sialyltransferase ST6GalNAc V (SIAT7E)	<i>Gallus gallus</i>	n.d.	AJ646877 CAG26706.1		
(fragment) $\alpha$ -2,8-sialyltransferase (GD3 Synthase), ST8Sia I	<i>Gallus gallus</i>	2.4.99.-	U73176 AAC28888.1	P79783	
$\alpha$ -2,8-sialyltransferase (SIAT8B)	<i>Gallus gallus</i>	n.d.	AJ699419 CAG27881.1		
$\alpha$ -2,8-sialyltransferase (SIAT8C)	<i>Gallus gallus</i>	n.d.	AJ699420 CAG27882.1		
$\alpha$ -2,8-sialyltransferase (SIAT8F)	<i>Gallus gallus</i>	n.d.	AJ699424 CAG27886.1		
$\alpha$ -2,8-sialyltransferase ST8Sia-V (SIAT8C)	<i>Gallus gallus</i>	n.d.	AJ704564 CAG28697.1		
$\beta$ -galactosamide $\alpha$ -2,6- sialyltransferase II (ST6Gal II)	<i>Gallus gallus</i>	n.d.	AJ627629 CAF29497.1		
GM3 synthase (SIAT9)	<i>Gallus gallus</i>	2.4.99.9	AY515255 AAS83519.1		
polysialyltransferase ST8Sia IV	<i>Gallus gallus</i>	2.4.99.-	AF008194 AAB95120.1	O42399	
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>Homo sapiens</i>	2.4.99.4	L29555 AAA36612.1 AF059321 AAC17874.1 L13972 AAC37574.1 AF155238 AAD39238.1 AF186191 AAG29876.1 BC018357 AAH18357.1 NM_003033 NP_003024.1 NM_173344 NP_775479.1	Q11201 Q60677 Q9UN51	
$\alpha$ -2,3-sialyltransferase ST3Gal II	<i>Homo sapiens</i>	2.4.99.4	U63090 AAB40389.1 BC036777 AAH36777.1 X96667 CAA65447.1 NM_006927 NP_008858.1	Q16842 O00654	
$\alpha$ -2,3-sialyltransferase ST3Gal III (SiaT6)	<i>Homo sapiens</i>	2.4.99.6	L23768 AAA35778.1 BC050380 AAH50380.1 AF425851 AAO13859.1 AF425852 AAO13860.1 AF425853 AAO13861.1 AF425854 AAO13862.1 AF425855 AAO13863.1 AF425856 AAO13864.1 AF425857 AAO13865.1 AF425858 AAO13866.1 AF425859 AAO13867.1 AF425860 AAO13868.1 AF425861 AAO13869.1 AF425862 AAO13870.1 AF425863 AAO13871.1 AF425864 AAO13872.1 AF425865 AAO13873.1 AF425866 AAO13874.1 AF425867 AAO13875.1 AY167992 AAO38806.1 AY167993 AAO38807.1 AY167994 AAO38808.1 AY167995 AAO38809.1 AY167996 AAO38810.1 AY167997 AAO38811.1 AY167998 AAO38812.1 NM_006279 NP_006270.1 NM_174964 NP_777624.1 NM_174965 NP_777625.1 NM_174966 NP_777626.1 NM_174967 NP_777627.1 NM_174969 NP_777629.1 NM_174970 NP_777630.1 NM_174972 NP_777632.1	Q11203 Q86UR6 Q86UR7 Q86UR8 Q86UR9 Q86US0 Q86US1 Q86US2 Q8IX43 Q8IX44 Q8IX45 Q8IX46 Q8IX47 Q8IX48 Q8IX49 Q8IX50 Q8IX51 Q8IX52 Q8IX53 Q8IX54 Q8IX55 Q8IX56 Q8IX57 Q8IX58	

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FIGURE 11D

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>Homo sapiens</i>	2.4.99.-	L23767 AAA16460.1 AF035249 AAC14162.1 BC010645 AAH10645.1 AY040826 AAK93790.1 AF516602 AAM66431.1 AF516603 AAM66432.1 AF516604 AAM66433.1 AF525084 AAM81378.1 X74570 CAA52662.1 CR456858 CAG33139.1 NM_006278 NP_006269.1	Q11206 O60497 Q96QQ9 Q8N6A6 Q8N6A7 Q8NFD3 Q8NFG7	
$\alpha$ -2,3-sialyltransferase ST3Gal VI	<i>Homo sapiens</i>	2.4.99.4	AF119391 AAD39131.1 BC023312 AAH123312.1 AB022918 BAA77609.1 AX877828 CAE89895.1 AX886023 CAF00161.1 NM_006100 NP_006091.1	Q9Y274	
$\alpha$ -2,6-sialyltransferase (ST6Gal II ; KIAA1877)	<i>Homo sapiens</i>	n.d.	BC008680 AAH08680.1 AB058780 BAB47506.1 AB059555 BAC24793.1 AJ512141 CAD54408.1 AX795193 CAE48260.1 AX795193 CAE48261.1 NM_032528 NP_115917.1	Q86Y44 Q8IUG7 Q96HE4 Q96JF0	
$\alpha$ -2,6-sialyltransferase (ST6GalNAC III)	<i>Homo sapiens</i>	n.d.	BC059363 AAH59363.1 AY358540 AAQ88904.1 AK091215 BAC03611.1 AJ507291 CAD45371.1 NM_152996 NP_694541.1	Q8N259 Q8NDV1	
$\alpha$ -2,6-sialyltransferase (ST6GalNac V)	<i>Homo sapiens</i>	n.d.	BC001201 AAH01201.1 AK056241 BAB71127.1 AL035409 CAB72344.1 AJ507292 CAD45372.1 NM_030965 NP_112227.1	Q9BVH7	
$\alpha$ -2,6-sialyltransferase (ST6GalNac II)	<i>Homo sapiens</i>	2.4.99.-	U14550 AAA52228.1 BC040455 AAH40455.1 AJ251053 CAB61434.1 NM_006456 NP_006447.1	Q9UJ37 Q12971	
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Homo sapiens</i>	2.4.99.1	BC031476 AAH31476.1 BC040009 AAH40009.1 A17362 CAA01327.1 A23699 CAA01686.1 X17247 CAA35111.1 X54363 CAA38246.1 X62822 CAA44634.1 NM_003032 NP_003023.1 NM_173216 NP_775323.1	P15907	
$\alpha$ -2,6-sialyltransferase ST6GalNac I	<i>Homo sapiens</i>	2.4.99.3	BC022462 AAH22462.1 AY096001 AAM22800.1 AY358918 AAQ89277.1 AK000113 BAA90953.1 Y11339 CAA72179.2 NM_018414 NP_060884.1	Q8TBJ6 Q9NSG7 Q9NXQ7	
$\alpha$ -2,8- polysialyltransferase ST8Sia IV	<i>Homo sapiens</i>	2.4.99.-	L41680 AAC41775.1 BC027866 AAH27866.1 BC053657 AAH53657.1 NM_005668 NP_005659.1	Q8N1F4 Q92187 Q92693	
$\alpha$ -2,8-sialyltransferase (GD3 synthase) ST8Sia I	<i>Homo sapiens</i>	2.4.99.8	L32867 AAA62366.1 L43494 AAC37586.1 BC046158 AAH46158.1 AAQ53140.1 AY569975 AAS75783.1 D26360 BAA05391.1 X77922 CAA54891.1 NM_003034 NP_003025.1	Q86X71 Q92185 Q93064	
$\alpha$ -2,8-sialyltransferase	<i>Homo sapiens</i>	2.4.99.-	L29556 AAA36613.1	Q92186	

**FIGURE 11E**

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
ST8Sia II			U82762 AAB51242.1 U33551 AAC24458.1 BC069584 AAH69584.1 NM_006011 NP_006002.1	Q92470 Q92746	
$\alpha$ -2,8-sialyltransferase	Homo sapiens	2.4.99.-	AF004668 AAB87642.1	Q43173	
ST8Sia III			AF003092 AAC15901.2 NM_015879 NP_056963.1	Q9NS41	
$\alpha$ -2,8-sialyltransferase	Homo sapiens	2.4.99.-	U91641 AAC51727.1 CR457037 CAG33318.1 NM_013305 NP_037437.1	O15466	
ST8Sia V			AC023295		
*ENSF00000020221 (fragment)		n.d.			
lactosylceramide $\alpha$ -2,3- sialyltransferase (ST3Gal V)	Homo sapiens	2.4.99.9	AF105026 AAD14634.1 AF119415 AAF66146.1 BC065936 AAH65936.1 AY152815 AAO16866.1 AAP65066 AAP65066.1 AY359105 AAQ89463.1 AB018356 BAA33950.1 AX876536 CAE89320.1 NM_003896 NP_003887.2	Q9UNP4 O94902	
N-acetylgalactosaminide $\alpha$ -2,6-sialyltransferase (ST6GalNAc VI)	Homo sapiens	2.4.99.-	BC006564 AAH06564.1 BC007802 AAH07802.1 BC016299 AAH16299.1 AY358672 AAQ89035.1 AB035173 BAA87035.1 AK023900 BAB14715.1 AJ507293 CAD45373.1 AX880950 CAE91145.1 CR457318 CAG33599.1 NM_013443 NP_038471.2	Q969X2 Q9H8A2 Q9ULB8	
N-acetylgalactosaminide $\alpha$ -2,6-sialyltransferase IV (ST6GalNAc IV)	Homo sapiens	2.4.99.-	AF127142 AAF00102.1 BC036705 AAH36705.1 - AAP63349.1 AB035172 BAA87034.1 AK000600 BAA91281.1 Y17461 CAB44354.1 AJ271734 CAC07404.1 AX061620 CAC24981.1 AX068265 CAC27250.1 AX969252 CAF14360.1 NM_014403 NP_055218.3 NM_175039 NP_778204.1	Q9H4F1 Q9NWU6 Q9UKU1 Q9ULB9 Q9Y3G3 Q9Y3G4	
ST8SIA-VI (fragment)	Homo sapiens	n.d.	AJ621583 CAF21722.1 XM_291725 XP_291725.2		
unnamed protein product	Homo sapiens	n.d.	AK021929 BAB13940.1 AX881696 CAE91353.1 AJ245699 CAB53394.1	Q9HAA9	
Gal $\beta$ -1,3/4-GlcNAc $\alpha$ - 2,3-sialyltransferase (ST3Gal III)	Mesocricetus auratus	2.4.99.6		Q9QXF6	

FIGURE 11F

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
Gal $\beta$ -1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase (ST3Gal IV)	<i>Mesocricetus auratus</i>	2.4.99.6	AJ245700 CAB53395.1	Q9QXF5	
GD3 synthase (fragment)	<i>Mesocricetus auratus</i>	n.d.	AF141657 AAD33879.1	Q9WUL1	
ST8Sia.I polysialyltransferase (ST8Sia IV)	<i>Mesocricetus auratus</i>	2.4.99.-	AJ245701 CAB53396.1	Q9QXF4	
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>St3gal1 Mus musculus</i>	2.4.99.4	AF214028 AAF60973.1 AK031344 BAC27356.1 AK078469 BAC37290.1 X73523 CAA51919.1 NM_009177 NP_033203.1	P54751 Q11202 Q9JL30	
$\alpha$ -2,3-sialyltransferase ST3Gal II	<i>St3gal2 Mus musculus</i>	2.4.99.4	BC015264 AAH15264.1 BC066064 AAH66064.1 AK034554 BAC28752.1 AK034863 BAC28859.1 AK053827 BAC35543.1 X76989 CAA54294.1 NM_009179 NP_033205.1 NM_178048 NP_835149.1	Q11204 Q8BPL0 Q8BSA0 Q8BSE9 Q91WH6	
$\alpha$ -2,3-sialyltransferase ST3Gal III	<i>St3gal3 Mus musculus</i>	2.4.99.-	BC006710 AAH06710.1 AK005053 BAB23779.1 AK013016 BAB28598.1 X84234 CAA59013.1 NM_009176 NP_033202.2	P97325 Q922X5 Q9CZ48 Q9DBB6	
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>St3gal4 Mus musculus</i>	2.4.99.4	BC011121 AAH111121.1 BC050773 AAH50773.1 D28941 BAA06068.1 AK008543 BAB25732.1 AB061305 BAB47508.1 X95809 CAA65076.1 NM_009178 NP_033204.2	P97354 Q61325 Q91Y74 Q921R5 Q9CVE8	
$\alpha$ -2,3-sialyltransferase ST3Gal VI	<i>St3gal6 Mus musculus</i>	2.4.99.4	AF119390 AAD39130.1 BC052338 AAH52338.1 AB063326 BAB79494.1 AK033562 BAC28360.1 AK041173 BAC30851.1 NM_018784 NP_061254	Q80UR7 Q8BLV1 Q8VIB3 Q9WVG2	
$\alpha$ -2,6-sialyltransferase ST6GalNAc II	<i>St6galnac2 Mus musculus</i>	2.4.99.-	NM_009180 6677963 BC010208 AAH10208.1 AB027198 BAB00637.1 AK004613 BAB23410.1 X93999 CAA63821.1 X94000 CAA63822.1 NM_009180 NP_033206.2	P70277 Q9DC24 Q9JJM5	
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>St6gal1 Mus musculus</i>	2.4.99.1	AF119390 AAD39130.1 BC027833 AAH27833.1 D16106 BAA03680.1 AK034768 BAG28828.1 AK084124 BAC39120.1 NM_145933 NP_666045.1	Q64685 Q8BM62 Q8K1L1	
$\alpha$ -2,6-sialyltransferase ST6Gal II	<i>St6gal2 Mus musculus</i>	n.d.	AK082566 BAC38534.1 AB095093 BAC87752.1 AK129462 BAC98272.1 NM_172829 NP_766417.1	Q8BUU4	
$\alpha$ -2,6-sialyltransferase ST6GalNAc I	<i>St6galnac1 Mus musculus</i>	2.4.99.3	Y11274 CAA72137.1 NM_011371 NP_035501.1	Q9QZ39 Q9JJP5	
$\alpha$ -2,6-sialyltransferase ST6GalNAc III	<i>St6galnac3 Mus musculus</i>	n.d.	BC058387 AAH58387.1 AK034804 BAC28836.1 Y11342 CAA72181.2 Y11343 CAB95031.1 NM_011372 NP_035502	Q9WUV2 Q9JHP5	
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV	<i>St6galnac4 Mus musculus</i>	2.4.99.7	BC056451 AAH56451.1 AK085730 BAC39523.1 AJ007310 CAA07446.1 Y15779 CAB43507.1	Q8C3J2 Q9JHP2 Q9R2B6 O88725	



FIGURE 11G

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
$\alpha$ -2,8-sialyltransferase (GD3 synthase) ST8Sia I	<i>Mus musculus</i>	2.4.99.8	Y15780 CAB33514.1 Y19055 CAB98946.1 Y19057 CAB98948.1 NM_011373 NP_035503.1 L38677 AAA91869.1 BC024821 AAH24821.1 AK046188 BAC32625.1 AK052444 BAC34994.1 X84235 CAA59014.1 AJ401102 CAC20706.1 NM_011374 NP_035504.1	Q9JHP0 Q9QUP9 Q9R2B5 Q64468 Q64687 Q8BL76 Q8BWI0 Q8K1C1 Q9EPK0	
$\alpha$ -2,8-sialyltransferase (ST8Sia VI)	<i>Mus musculus</i>	n.d.	AB059554 BAC01265.1 AK085105 BAC39367.1 NM_145838 NP_665837.1	Q8BI43 Q8K4T1	
$\alpha$ -2,8-sialyltransferase ST8Sia II	<i>Mus musculus</i>	2.4.99.-	X83562 CAA58548.1 X99646 CAA67965.1 X99647 CAA67965.1 X99648 CAA67965.1 X99649 CAA67965.1 X99650 CAA67965.1 X99651 CAA67965.1 NM_009181 NP_033207.1	O35696	
$\alpha$ -2,8-sialyltransferase ST8Sia IV	<i>Mus musculus</i>	2.4.99.8	BC060112 AAH60112.1 AK003690 BAB22941.1 AK041723 BAC31044.1 AJ223956 CAA11685.1 X86000 CAA59992.1 Y09484 CAA70692.1 NM_009183 NP_033209.1	Q64692 Q8BY70	
$\alpha$ -2,8-sialyltransferase ST8Sia V	<i>Mus musculus</i>	2.4.99.-	BC034855 AAH34855.1 AK078670 BAC37354.1 X98014 CAA66642.1 X98014 CAA66643.1 X98014 CAA66644.1 NM_013666 NP_038694.1 NM_153124 NP_694764.1 NM_177416 NP_803135.1	P70126 P70127 P70128 Q8BJW0 Q8JZQ3	
$\alpha$ -2,8-sialyltransferase ST8Sia III	<i>Mus musculus</i>	2.4.99.-	BC075645 AAH75645.1 AK015874 BAB30012.1 X80502 CAA56665.1 NM_009182 NP_033208.1	Q64689 Q9CUJ6	
GD1 synthase (ST6GalNAc V)	<i>Mus musculus</i>	n.d.	BC055737 AAH55737.1 AB030836 BAA85747.1 AB028840 BAA89292.1 AK034387 BAC28693.1 AK038434 BAC29997.1 AK042683 BAC31331.1 NM_012028 NP_036158.2	Q8CAM7 Q8CBX1 Q9QYJ1 Q9R0K6	
GM3 synthase ( $\alpha$ -2,3-sialyltransferase) ST3Gal V	<i>Mus musculus</i>	2.4.99.9	AF119416 AAF66147.1 AF124121 AAP65063.1 AB018048 BAA33491.1 AB013302 BAA76467.1 AK012961 BAB28571.1 AY15003 CAA75235.1 NM_011375 NP_035505.1	O88829 Q9CZ65 Q9QWF9	
N-acetylgalactosaminide $\alpha$ -2,6-sialyltransferase (ST6GalNAc VI)	<i>Mus musculus</i>	2.4.99.-	BC036985 AAH36985.1 AB035174 BAA87036.1 AB035123 BAA95940.1 AK030648 BAC27064.1 NM_016973 NP_058669.1	Q8CDC3 Q8JZW3 Q9JMN5 Q9R0G9	
M138L	<i>Myxoma virus</i>	n.d.	U46578 AAD00069.1 AF170726 AAE61323.1 NC_001132 AAE61326.1 AAE15026.1 NP_051852.1		
$\alpha$ -2,3-sialyltransferase	<i>Oncorhynchus</i>	n.d.	AJ585760 CAE51384.1		

FIGURE 11H

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
(ST3Gal-I) $\alpha$ -2,6-sialyltransferase (Siat1)	<i>mykiss</i> <i>Oncorhynchus mykiss</i>	n.d.	AJ620649 CAF05848.1		
$\alpha$ -2,8-polysialyltransferase IV (ST8Sia IV)	<i>mykiss</i>	n.d.	AB094402 BAC77411.1	Q7T2X5	
GalNAc $\alpha$ -2,6-sialyltransferase (RtST6GalNAc)	<i>Oncorhynchus mykiss</i>	n.d.	AB097943 BAC77520.1	Q7T2X4	
$\alpha$ -2,3-sialyltransferase ST3Gal IV OJ1217_F02.7	<i>Oryctolagus cuniculus</i>	2.4.99.-	AF121967 AAF28871.1	Q9N257	
	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AP004084 BAD07616.1		
OSJNBa0043L24.2 or OSJNBb0002J11.9	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AL731626 CAD41185.1 AL662969 CAE04714.1		
P0683f02.18 or P0489B03.1	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AP003289 BAB63715.1 AP003794 BAB90552.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Oryzias latipes</i>	n.d.	AJ646876 CAG26705.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Pan troglodytes</i>	n.d.	AJ744803 CAG32839.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5)	<i>Pan troglodytes</i>	n.d.	AJ744804 CAG32840.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Pan troglodytes</i>	n.d.	AJ626819 CAF25177.1		
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat4c)	<i>Pan troglodytes</i>	n.d.	AJ626824 CAF25182.1		
$\alpha$ -2,3-sialyltransferase ST3Gal VI (Siat10)	<i>Pan troglodytes</i>	n.d.	AJ744808 CAG32844.1		
$\alpha$ -2,6-sialyltransferase (Siat7A)	<i>Pan troglodytes</i>	n.d.	AJ748740 CAG38615.1		
$\alpha$ -2,6-sialyltransferase (Siat7B)	<i>Pan troglodytes</i>	n.d.	AJ748741 CAG38616.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (Siat7C)	<i>Pan troglodytes</i>	n.d.	AJ634454 CAG25676.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	<i>Pan troglodytes</i>	n.d.	AJ646870 CAG26699.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E)	<i>Pan troglodytes</i>	n.d.	AJ646875 CAG26704.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Pan troglodytes</i>	n.d.	AJ646882 CAG26711.1		
$\alpha$ -2,8-sialyltransferase 8A (Siat8A)	<i>Pan troglodytes</i>	2.4.99.8	AJ697658 CAG26896.1		
$\alpha$ -2,8-sialyltransferase 8B (Siat8B)	<i>Pan troglodytes</i>	n.d.	AJ697659 CAG26897.1		
$\alpha$ -2,8-sialyltransferase 8C (Siat8C)	<i>Pan troglodytes</i>	n.d.	AJ697660 CAG26898.1		
$\alpha$ -2,8-sialyltransferase 8D (Siat8D)	<i>Pan troglodytes</i>	n.d.	AJ697661 CAG26899.1		
$\alpha$ -2,8-sialyltransferase 8E (Siat8E)	<i>Pan troglodytes</i>	n.d.	AJ697662 CAG26900.1		
$\alpha$ -2,8-sialyltransferase 8F (Siat8F)	<i>Pan troglodytes</i>	n.d.	AJ697663 CAG26901.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase I (ST6Gal I; Siat1)	<i>Pan troglodytes</i>	2.4.99.1	AJ627624 CAF29492.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II (ST6Gal II)	<i>Pan troglodytes</i>	n.d.	AJ627625 CAF29493.1		
GM3 synthase ST3Gal V	<i>Pan troglodytes</i>	n.d.	AJ744807 CAG32843.1		

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FIGURE 111

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
(Siat9)					
S138L	<i>Rabbit fibroma virus Kasza</i>	n.d.	NC_001266 NP_052025		
$\alpha$ -2,3-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.6	M97754 AAA42146.1	Q02734	
ST3Gal III			NM_031697 NP_113885.1		
$\alpha$ -2,3-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ626825 CAF25183.1		
ST3Gal IV (Siat4c)					
$\alpha$ -2,3-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ626743 CAF25053.1		
ST3Gal VI					
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.-	X76988 CAA54293.1	Q11205	
ST3Gal II			NM_031695 NP_113883.1		
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.1	M18769 AAA41196.1	P13721	
ST6Gal I			M83143 AAB07233.1		
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ634458 CAG25684.1		
ST6GalNAc I (Siat7A)					
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ634457 CAG25679.1		
ST6GalNAc II (Siat7B)					
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.-	L29554 AAC42086.1	Q64686	
ST6GalNAc III			BC072501 AAH72501.1		
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	NM_019123 NP_061996.1		
ST6GalNAc IV (Siat7D)			AJ646871 CAG26700.1		
(fragment)					
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ646872 CAG26701.1		
ST6GalNAc V (Siat7E)					
$\alpha$ -2,6-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ646881 CAG26710.1		
ST6GalNAc VI (Siat7F)					
(fragment)					
$\alpha$ -2,8-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.-	U53883 AAC27541.1	P70554	
(GD3 synthase) ST8Sia I			D45255 BAA08213.1	P97713	
$\alpha$ -2,8-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ699422 CAG27884.1		
(SIAT8E)					
$\alpha$ -2,8-sialyltransferase	<i>Rattus norvegicus</i>	n.d.	AJ699423 CAG27885.1		
(SIAT8F)					
$\alpha$ -2,8-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.-	L13445 AAA42147.1	Q07977	
ST8Sia II			NM_057156 NP_476497.1	Q64688	
$\alpha$ -2,8-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.-	U55938 AAB50061.1	P97877	
ST8Sia III			NM_013029 NP_037161.1		
$\alpha$ -2,8-sialyltransferase	<i>Rattus norvegicus</i>	2.4.99.-	U90215 AAB49989.1	O08563	
ST8Sia IV					
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II	<i>Rattus norvegicus</i>	n.d.	AJ627626 CAF29494.1		
(ST6Gal II)					
GM3 synthase ST3Gal V	<i>Rattus norvegicus</i>	n.d.	AB018049 BAA33492.1	O88830	
$\alpha$ -2,3-sialyltransferase			NM_031337 NP_112627.1		
ST3Gal I (Siat4A)	<i>Rattus norvegicus</i>	n.d.	AJ748840 CAG44449.1		
$\alpha$ -2,3-sialyltransferase	<i>Silurana tropicalis</i>	n.d.	AJ585763 CAE51387.1		
(ST3Gal-II)					
$\alpha$ -2,6-sialyltransferase	<i>Silurana tropicalis</i>	n.d.	AJ620650 CAF05849.1		
(Siat7b)					
$\alpha$ -2,6-sialyltransferase	<i>Strongylocentrotus purpuratus</i>	n.d.	AJ699425 CAG27887.1		
(ST6galnac)					
$\alpha$ -2,3-sialyltransferase	<i>Sus scrofa</i>	n.d.	AJ585765 CAE51389.1		
(ST3GAL-III)					
$\alpha$ -2,3-sialyltransferase	<i>Sus scrofa</i>	n.d.	AJ584674 CAE48299.1		
(ST3GAL-IV)					
$\alpha$ -2,3-sialyltransferase	<i>Sus scrofa</i>	2.4.99.4	M97753 AAA31125.1	Q02745	
ST3Gal I					
$\alpha$ -2,6-sialyltransferase	<i>Sus scrofa</i>	2.4.99.1	AF136746 AAD33059.1	Q9XSG8	
(fragment) ST6Gal I					
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase	<i>Sus scrofa</i>	n.d.	AJ620948 CAF06585.2		
(ST6GalNAc-V)					
sialyltransferase	<i>sus scrofa</i>	n.d.	AF041031 AAC15633.1	O62717	
(fragment) ST6Gal I					

FIGURE 11J

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
ST6GalNAc-V	<i>Sus scrofa</i>	n.d.	AJ620948 CAF06585.1		
$\alpha$ -2,3-sialyltransferase (Siat5-r)	<i>Takifugu rubripes</i>	n.d.	AJ744805 CAG32841.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Takifugu rubripes</i>	n.d.	AJ626816 CAF25174.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ626817 CAF25175.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Takifugu rubripes</i>	n.d.	AJ626818 CAF25176.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I (Siat1)	<i>Takifugu rubripes</i>	n.d.	AJ744800 CAG32836.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Takifugu rubripes</i>	n.d.	AJ634460 CAG25681.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II B (Siat7B-related)	<i>Takifugu rubripes</i>	n.d.	AJ634461 CAG25682.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (Siat7C) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ634456 CAG25678.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	<i>Takifugu rubripes</i>	2.4.99.3	Y17466 CAB44338.1 AJ646869 CAG26698.1	Q9W6U6	
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ646873 CAG26702.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ646880 CAG26709.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715534 CAG29373.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715538 CAG29377.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715541 CAG29380.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IIIr (Siat 8Cr)	<i>Takifugu rubripes</i>	n.d.	AJ715542 CAG29381.1		
$\alpha$ -2,8-sialyltransferase ST8Sia V (Siat 8E) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715547 CAG29386.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715549 CAG29388.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VIr (Siat 8Fr)	<i>Takifugu rubripes</i>	n.d.	AJ715550 CAG29389.1		
$\alpha$ -2,3-sialyltransferase (Siat5-r)	<i>Tetraodon nigroviridis</i>	n.d.	AJ744806 CAG32842.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Tetraodon nigroviridis</i>	n.d.	AJ744802 CAG32838.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Tetraodon nigroviridis</i>	n.d.	AJ626822 CAF25180.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Tetraodon nigroviridis</i>	n.d.	AJ634462 CAG25683.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ646879 CAG26708.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715536 CAG29375.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715537 CAG29376.1		
$\alpha$ -2,8-sialyltransferase	<i>Tetraodon</i>	n.d.	AJ715539 CAG29378.1		

FIGURE 11K

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
ST8Sia III (Siat 8C) (fragment)	<i>nigroviridis</i>				
$\alpha$ -2,8-sialyltransferase	<i>Tetraodon</i>	n.d.	AJ715540 CAG29379.1		
ST8Sia IIIr (Siat 8Cr) (fragment)	<i>nigroviridis</i>				
$\alpha$ -2,8-sialyltransferase	<i>Tetraodon</i>	n.d.	AJ715548 CAG29387.1		
ST8Sia V (Siat 8E) (fragment)	<i>nigroviridis</i>				
$\alpha$ -2,3-sialyltransferase (St3Gal-II)	<i>Xenopus laevis</i>	n.d.	AJ585762 CAE51386.1		
$\alpha$ -2,3-sialyltransferase (St3Gal-VI)	<i>Xenopus laevis</i>	n.d.	AJ585766 CAE51390.1		
$\alpha$ -2,3-sialyltransferase St3Gal-III (Siat6)	<i>Xenopus laevis</i>	n.d.	AJ585764 CAE51388.1		
$\alpha$ -2,8-polysialyltransferase	<i>Xenopus laevis</i>	2.4.99.-	AJ626823 CAF25181.1		
$\alpha$ -2,8-sialyltransferase ST8Sia-I (Siat8A;GD3 synthase)	<i>Xenopus laevis</i>	n.d.	AB007468 BAA32617.1 O93234		
Unknown (protein for MGC:81265)	<i>Xenopus laevis</i>	n.d.	AY272056 AAQ16162.1		
$\alpha$ -2,3-sialyltransferase (3Gal-VI)	<i>Xenopus tropicalis</i>	n.d.	AY272057 AAQ16163.1		
$\alpha$ -2,3-sialyltransferase (Siat4c)	<i>Xenopus tropicalis</i>	n.d.	AJ626823 CAF25181.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Xenopus tropicalis</i>	n.d.	AJ626744 CAF25054.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Xenopus tropicalis</i>	n.d.	AJ622908 CAF22058.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II (ST6Gal II)	<i>Xenopus tropicalis</i>	n.d.	AJ646878 CAG26707.1		
sialyltransferase St8Sial	<i>Xenopus tropicalis</i>	n.d.	AJ715544 CAG29383.1		
poly- $\alpha$ -2,8-sialosyl sialyltransferase (NeuS)	<i>Escherichia coli</i> K1	2.4.-.-	M76370 AAA24213.1	Q57269	
polysialyltransferase	<i>Escherichia coli</i> K92	2.4.-.-	X60598 CAA43053.1		
			M88479 AAA24215.1	Q47404	
$\alpha$ -2,8 polysialyltransferase SiaD	<i>Neisseria meningitidis</i> B1940	2.4.-.-	M95053 AAA20478.1	Q51281	
SynE	<i>Neisseria meningitidis</i> FAM18	n.d.	X78068 CAA54985.1	Q51145	
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M1019	n.d.	AY234192 AAO85290.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M209	n.d.	AY281046 AAP34769.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M3045	n.d.	AY281044 AAP34767.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M3315	n.d.	AY234191 AAO85289.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M3515	n.d.	AY281047 AAP34770.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M4211	n.d.	AY234190 AAO85288.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M4642	n.d.	AY281048 AAP34771.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M5177	n.d.	AY234193 AAO85291.1		
SiaD	<i>Neisseria meningitidis</i> M5178	n.d.	AY281043 AAP34766.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M980	n.d.	AY281045 AAP34768.1		
NMB0067	<i>Neisseria meningitidis</i> MC58	n.d.	NC_003112 NP_273131		

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FIGURE 11L

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
Lst	<i>Aeromonas punctata</i> Sch3	n.d.	AF126256 AAC56624.1		
ORF2	<i>Haemophilus influenzae</i> A2	n.d.	M94855 AAA24979.1		
HI1699	<i>Haemophilus influenzae</i> Rd	n.d.	U32842 AAC23345.1 @48211 NC_000907 NP_239841.1		
$\alpha$ -2,3-sialyltransferase	<i>Neisseria gonorrhoeae</i> F62	2.4.99.4	U60664 AAC44539.1 AAE67205.1	P72074	
$\alpha$ -2,3-sialyltransferase	<i>Neisseria meningitidis</i> 126E, NRCC 4010	2.4.99.4	U60662 AAC44544.1		
$\alpha$ -2,3-sialyltransferase	<i>Neisseria meningitidis</i> 406Y, NRCC 4030	2.4.99.4	U60661 AAC44543.1		
$\alpha$ -2,3-sialyltransferase (NMB0922)	<i>Neisseria meningitidis</i> MC58	2.4.99.4	U60660 AAC44541.1 AE002443 AAF41330.1 NC_003112 NP_273962.1	P72097	
NMA1118	<i>Neisseria meningitidis</i> Z2491	n.d.	AL162755 CAB84380.1 NC_003116 NP_283887.1	Q9JUV5	
PM0508	<i>Pasteurella multocida</i> PM70	n.d.	AE006086 AAK02592.1 NC_002663 NP_245445.1	Q9CNC4	
WaaH	<i>Salmonella enterica</i> SARB25	n.d.	AF519787 AAM82550.1	Q8KS93	
WaaH	<i>Salmonella enterica</i> SARB3	n.d.	AF519788 AAM82551.1	Q8KS92	
WaaH	<i>Salmonella enterica</i> SARB39	n.d.	AF519789 AAM82552.1		
WaaH	<i>Salmonella enterica</i> SARB53	n.d.	AF519790 AAM82553.1		
WaaH	<i>Salmonella enterica</i> SARB57	n.d.	AF519791 AAM82554.1	Q8KS91	
WaaH	<i>Salmonella enterica</i> SARB71	n.d.	AF519793 AAM82556.1	Q8KS89	
WaaH	<i>Salmonella enterica</i> SARB8	n.d.	AF519792 AAM82555.1	Q8KS90	
WaaH	<i>Salmonella enterica</i> SARC10V	n.d.	AF519779 AAM88840.1	Q8KS95	
WaaH (fragment)	<i>Salmonella enterica</i> SARC12	n.d.	AF519781 AAM88842.1		
WaaH (fragment)	<i>Salmonella enterica</i> SARC13I	n.d.	AF519782 AAM88843.1	Q8KS98	
WaaH (fragment)	<i>Salmonella enterica</i> SARC14I	n.d.	AF519783 AAM88844.1	Q8KS97	
WaaH	<i>Salmonella enterica</i> SARC15II	n.d.	AF519784 AAM88845.1	Q8KS96	
WaaH	<i>Salmonella enterica</i> SARC16II	n.d.	AF519785 AAM88846.1	Q8KS95	

FIGURE 11M

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
WaaH (fragment)	<i>Salmonella enterica</i> SARC3I	n.d.	AF519772 AAM88834.1	Q8KSA4	
WaaH (fragment)	<i>Salmonella enterica</i> SARC4I	n.d.	AF519773 AAM88835.1	Q8KSA3	
WaaH	<i>Salmonella enterica</i> SARC5IIa	n.d.	AF519774 AAM88836.1		
WaaH	<i>Salmonella enterica</i> SARC6IIa	n.d.	AF519775 AAM88837.1	Q8KSA2	
WaaH	<i>Salmonella enterica</i> SARC8	n.d.	AF519777 AAM88838.1	Q8KSA1	
WaaH	<i>Salmonella enterica</i> SARC9V	n.d.	AF519778 AAM88839.1	Q8KSA0	
UDP-glucose: $\alpha$ -1,2-glucosyltransferase (WaaH)	<i>Salmonella enterica</i> subsp. <i>anzoniae</i> SARC 5	2.4.1.-	AF511116 AAM48166.1		
bifunctional $\alpha$ -2,3/-2,8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43449	n.d.	AF401529 AAL06004.1	Q93CZ5	
Cst	<i>Campylobacter jejuni</i> 81-176	n.d.	AF305571 AAL09368.1		
$\alpha$ -2,3-sialyltransferase (Cst-III)	<i>Campylobacter jejuni</i> ATCC 43429	2.4.99.-	AY044156 AAK73183.1		
$\alpha$ -2,3-sialyltransferase (Cst-III)	<i>Campylobacter jejuni</i> ATCC 43430	2.4.99.-	AF400047 AAK85419.1		
$\alpha$ -2,3-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43432	2.4.99.-	AF215659 AAG43979.1	Q9F0M9	
$\alpha$ -2,3/-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> ATCC 43438	n.d.	AF400048 AAK91725.1	Q93MQ0	
$\alpha$ -2,3-sialyltransferase cst-II	<i>Campylobacter jejuni</i> ATCC 43446	2.4.99.-	AF167344 AAF34137.1		
$\alpha$ -2,3-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43456	2.4.99.-	AF401528 AAL05990.1	Q93D05	
$\alpha$ -2,3/- $\alpha$ -2,8-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> ATCC 43460	2.4.99.-	AY044868 AAK96001.1	Q938X6	
$\alpha$ -2,3-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 700297	n.d.	AF216647 AAL36462.1		
ORF	<i>Campylobacter jejuni</i> GB11	n.d.	AY422197 AAR82875.1		
$\alpha$ -2,3-sialyltransferase cstIII	<i>Campylobacter jejuni</i> MSC57360	2.4.99.-	AF195055 AAG29922.1		
$\alpha$ -2,3-sialyltransferase cstIII Cj1140	<i>Campylobacter jejuni</i> NCTC 11168	2.4.99.-	AL139077 CAB73395.1	Q9PNF4	
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (cstII)	<i>Campylobacter jejuni</i> O:10	n.d.	-AAO96669.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)	<i>Campylobacter jejuni</i> O:19	n.d.	AX934427 CAF04167.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)	<i>Campylobacter jejuni</i> O:36	n.d.	AX934431 CAF04169.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)	<i>Campylobacter jejuni</i> O:4	n.d.	AX934436 CAF04171.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)	<i>Campylobacter jejuni</i> O:41	n.d.	AX934434 CAF04170.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)		n.d.	-AAO96670.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)		n.d.	-AAT17967.1		
$\alpha$ -2,3-sialyltransferase cst-I	<i>Campylobacter jejuni</i> OH4384	2.4.99.-	AX934429 CAF04168.1		
bifunctional $\alpha$ -2,3/-2,8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> OH4384	2.4.99.-	AF130466 AAF13495.1	Q9RGF1	
			AX934425 CAF04166.1		
			AF130984 AAF31771.1		1RO7 C
					1RO8 A

FIGURE 11N

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
HI0352 (fragment)	<i>Haemophilus influenzae</i>	n.d.	U32720 AAC22019.1	P24324	
	Rd		X57315 CAA40567.1		
PM1174	<i>Pasteurella multocida</i>	n.d.	NC_000907 NP_438516.1	Q9CLP3	
	PM70		AE006157 AAK03258.1		
Sequence 10 from patent US 6503744	Unknown.	n.d.	NC_002663 NP_246111.1		
Sequence 10 from patent US 6699705	Unknown.	n.d.	- AAO96672.1		
Sequence 12 from patent US 6699705	Unknown.	n.d.	- AAT17970.1		
Sequence 2 from patent US 6709834	Unknown.	n.d.	- AAT23232.1		
Sequence 3 from patent US 6503744	Unknown.	n.d.	- AAO96668.1		
Sequence 3 from patent US 6699705	Unknown.	n.d.	- AAT17965.1		
Sequence 34 from patent US 6503744	Unknown.	n.d.	- AAO96684.1		
Sequence 35 from patent US 6503744 (fragment)	Unknown.	n.d.	- AAO96685.1		
Sequence 48 from patent US 6699705	Unknown.	n.d.	- AAS36262.1		
Sequence 5 from patent US 6699705	Unknown.	n.d.	- AAT17988.1		
Sequence 9 from patent US 6503744	Unknown.	n.d.	- AAT17966.1		
			- AAO96671.1		



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